



Supplementary Figure 1: Technical validation of HELP data by bisulphite MassArray. (A) Bisulphite MassArray analysis was performed for samples from eight different rats using four loci, two each representing constitutively hypo- and hypermethylated sites ($n=32$, filled circles). HELP data as $\log_2(\text{HpaII}/\text{MspI})$ ratios are shown along the x-axis, with increased methylation on the left of the distribution. Bisulphite MassArray data for the same loci are plotted along the y-axis, from 0% (hypomethylated) to 100% (methylated). (B) The distribution of $\log_2(\text{HpaII}/\text{MspI})$ ratios, shown as an averaged density across all microarray experiments. The x-axis corresponds to the same axis in panel (A); however, the y-axis in this lower panel is not quantified as the density distribution is demonstrated in relative units. The bimodal distribution represents a hypomethylated population of loci (positive logratios) and a hypermethylated population (negative logratios). The vertical dashed line indicates the zero threshold which we use to discriminate hyper- and hypomethylated loci.